

Figure 1A

1 CCACGCGTCCGAACATGGGCTGAGAGCCCCCAAGAGCATCTCTAAGACCGGAGTGGGC 60  
61 AGGGACCCGGGCCTCTGAGGGGCTCAGGCTCCAGGCCGAACTGCACGCGGTGCTGGCG 120  
121 TCAGGCCCAGGCCAGCTACGCCTCCACGGCCTCCCTAATCGCCATTCTGGGGCTTGCG 180  
181 GGAGCACCTGGGAGGCTCCACCCGAGCCAGACACTGCCTGCCCCACGCCCTCCAGGA 240  
241 CCTCGAAGGAGAAGGAAATCGGGACTGGCCCAGCGTCCCGTGCTCTAGAAGCGGGCTA 300  
301 CTGCCCCGTCCCAAGCAGGGGAGGAGGACGAGCGAGGGCGTCACTCATCTGTCCCCCGC 360  
361 GGAAGGATGAGGAAGCTCTGTTTACCTAAATGAAAAGCTTTCTAGGAGGAAGTCTTAAGT 420  
421 GAACAATGATGCATGAGGATGCAATCTTACAGACACAGGGGTCTCCCTATGTTGTTCAAG 480  
481 CTGGTCTCGAACTCCTGGCCTCAAGTGATCCTCCTGCCTCGACCTCTCAAAGCTCTGGTA 540  
541 TTATAGGCAAGGAGCCCAGTGATAACAAATGGCTGTAGATGCTTTTCTCCATCAAGCTT 600  
601 CCAGGAGGAGATGAGATGGAGCCCATCGCTGAGCCAAGAATTCTAATTTCATCCCTTTGG 660  
661 TCTTTGTTCATGCTGTGTTCTGCCTGGAATATTCTCCATCTTCTTGCCTGGAAAAGTAT 720  
721 TACTTACTGAAACCTTGAAGCCACTACCTTCTCTAAACATTGACAATGCATAACCATTG 780  
781 CCGAGCGTTCTTCCCCGACTGCATCCGTTTAGTCTACTGAGAGGCAGCTCAGCGTTCCC 840  
841 AAGGAGACAGATGTCTAGCTTTGCTCTTTCTGTCTGTGTGATGCTGGAGAATCGATATGC 900  
901 CCTTGGGCCTCCATCTCCATCTGTAAAACAAGGGCATCAGATACCCACCTGGTGGCCCG 960  
961 TCCTCACTTGGAACCACTCAACATGCCTTCTGGAAGTCTCTCTTGTCACCTCAAGAAAA 1020  
1021 GATCCCCAGGAAACCTACAGGGACTATGTCCGCAGGAAATCCGGCTCATGGAAGACCGC 1080  
1081 AATGCGCGCCTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTCCTGTGGTG 1140  
1141 AAGGAGCACTCAAACCCCATGCAGGTCCAGCAGCAGCTTCTGGACACAGGCCGGGGACAC 1200

Figure 1B

1201	GCGAGGACCGTGGGACACCAGGCTAGCCCCATCAAGATAGAGACCCTCTTTGAGCCAGAC	1260
1261	GAGGAGCGCCCCGAGCCACCGCGCACCGTGGTCATGCAAGGCGCGGCAGGGATAGGGAGA	1320
1		M 1
1321	TGAACCAGAGTGCCACGGAATGCAGCATGCAAGACCTCATCTTCAGCTGCTGGCCTGAGC	1380
2	N Q S A T E C S M Q D I F S C W P E P	21
1381	CCAGCGCGCTCTCCAGGAGCTCATCCGAGTTCCCGAGCGCTCCTTTTCATCATCGACG	1440
22	S A P L Q E L I R V P E R L F I I D G	41
1441	GCTTCGATGAGCTCAAGCCTTCTTTCCACGATCCTCAGGACCCCTGGTGCCTCTGCTGGG	1500
42	F D E L K P S F H D P Q G P W C L C W E	61
1501	AGGAGAAACGGCCCCACGAGCTGCTTCTTAACAGCTTAATTCGGAAGAAGCTGCTCCCTG	1560
62	E K R P T E L N S I R K K L P E	81
1561	AGCTATCTTTGCTCATCACACACGCGCCACGCTTTGGAGAAGCTCCACCGTCTGCTGG	1620
82	L S L I T T R P T A L E K L H R L E	101
1621	AGCACCCCAGGCATGTGGAGATCCTGGGCTTCTCTGAGGCAGAAAGGAAGGAATACTTCT	1680
102	H P R H V E I L G F S E A E R K E Y F Y	121
1681	ACAAGTATTTCCACAATGCAGAGCAGCGCGGCAAGTCTTCAATTACGTGAGGGACAACG	1740
122	K Y F H N A E Q A G Q V F N Y V R D N E	141
1741	AGCCTCTCTTACCATGTGCTTCGTCCTCCCTGGTGTGCTGGGTGGTGTACCTGCCTCC	1800
142	P L F T M C F V P L V C W V V C T C L Q	161
1801	AGCAGCAGCTGGAGGGTGGGGGGCTGTTGAGACAGACGTCCAGGACCACCACTGCAGTGT	1860
162	Q Q L E G G G L L R Q T S R T T T A V Y	181
1861	ACATGCTCTACCTGCTGAGTCTGATGCAACCCAAGCCGGGGGGCGCGCTCCAGCCCC	1920
182	M L Y L L S L M Q P K P G A P R L Q P P	201
1921	CACCCAACCAGAGAGGGTGTGCTCCTTGGCGGCAGATGGGCTCTGGAATCAGAAAATCC	1980
202	P N Q R G C S L A A D G L W N Q K I L	221
1981	TATTTGAGGAGCAGGACCTCCGGAAGCACGGCCTAGACGGGGAAGACGTCTCTGCCTTCC	2040
222	F E E Q D L R K H G D G E D V S A F L	241
2041	TCAACATGAACATCTTCCAGAAGGACATCAACTGTGAGAGGAGCTTCTGGCACTCACCA	2100
242	N M N I F Q K D I N C E R S F L A L T S	261

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0

Figure 1C

2101	CCCCGCTTCCTGTTTGGACTCCTGAACGAGGAGACCAGGAGCCACCTGGAGAAGAGTCTCT	2160
262	R F <u>F</u> F G <u>F</u> <u>F</u> N E E T R S H L E K S L C	281
2161	GCTGGAAGGTCTCGCCGCACATCAAGATGGACCTGTTGCAGTGGATCCAAAGCAAAGCTC	2220
282	W K V S P H I K M D <u>F</u> L Q W I Q S K A Q	301
2221	AGAGCGACGGCTCCACCCTGCAGCAGGGCTCCTTGGAGTTCTTCAGCTGCTTGTACGAGA	2280
302	S D G S T L Q Q G S L E F F S <u>C</u> L Y E I	321
2281	TCCAGGAGGAGGAGTTTATCCAGCAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCA	2340
322	Q E E E F I Q Q A L S H F Q V I V V S N	341
2341	ACATTGCCTCCAAGATGGAGCACATGGTCTCCTCGTTCTGTCTGAAGCGCTGCAGGAGCG	2400
342	I A S K M E H M V S S F C L K R C R S A	361
2401	CCCAGGTGCTGCACTTGTATGGCGCCACCTACAGCGGGACGGGGAAGACCGCGCGAGGT	2460
362	Q V <u>F</u> H <u>F</u> Y G A T Y S A D G E D R A R C	381
2461	GCTCCGCAGGAGCGCACACGCTGTTGGTGCAGCTACCAGAGAGGACCGTTCTGCTGGACG	2520
382	S A G A H T L L V Q L P E R T V L L D A	401
2521	CCTACAGTGAACATCTGGCAGCGGCCCTGTGCACCAATCCAAACCTGATAGAGCTGTCTC	2580
402	Y S E H <u>F</u> A A A <u>F</u> C T N P N L I E <u>F</u> S <u>F</u>	421
2581	TGTACCGAAATGCCCTGGGCAGCGGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACC	2640
422	Y R N A L G S R G V K L L C Q G <u>F</u> R H P	441
2641	CCAACTGCAAACCTTCAGAACCTGAGGTAAAATTATCATATATAACATGATATTTTGAAA	2700
442	N <u>C</u> K <u>F</u> Q N <u>F</u> R *	449
2701	TAAATATATTGGCCAGGTATGATGGCTCACGCCTGTAATTCCAGCACTTTGGGAGGCCCA	2760
2761	GATGGGGAGGATCACTTGACCCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCC	2820
2821	CATCTCTACTAAAAATACCAAAATGAGCCAGGCATGGTGGCACACGTCTGTAAGCCCAGC	2880
2881	TACTCAGGAGGCCAAGGCAGGAGGATTGCTTCAACCCAGGAGGCAGAGGTTGTGGCTGAA	2940
2941	GAGGTGCCGCATCTCCAGCTCAGCCTGCGAGGACCTCTCTGCAGCTCTCATAGCCAATAA	3000
3001	GAATTTGACAAGGATGGATCTCAGTGGCAACGGCGTTGGATTCCCAGGCATGATGCTGCT	3060
3061	TGCGAGGGCCTGCGGCATCCCCAATGCAGGCTGCAGATGATTGAGTTGAGGAAGTGTC	3120

Figure 1D

3121 GCTGGAGTCCGGGGCTTGTCTCAGGAGATGGCTTCTGTGCTTGGCACCAACCCACATCTGGT 3180  
 3181 TGAGTTGGACCTGACAGGAAATGCACCTGGAGGATTTGGGCCTGAGGTTACTATGCCAGGG 3240  
 3241 ACTGAGGCACCCAGTCTGCAGACTACGGACTTTGTGGCTGAAGATCTGCCGCCTCACTGC 3300  
 3301 TGCTGCCTGTGACGAGCTGGCCTCAACTCTCAGTGTGAACCAGAGCCTGAGAGAGCTGGA 3360  
 3361 CCTGAGCCTGAATGAGCTGGGGGACCTCGGGGTGCTGCTGCTGTGTGAGGGCCTCAGGCA 3420  
 3421 TCCCACGTGCAAGCTCCAGACCTGCGGTGAGTCCCGTTTGTCTCACCACGCTAGGAGTC 3480  
 3481 CCAATCCATGAACGCGACCCCTCTCACCTGGGACCACGGAGGCCAGGTTGTCTCTGCTCCT 3540  
 3541 AAATCTAGCTACTACATCAGCCCTTTTTTTTTTTTTTTTGGAGACTCCCAAGTAGCTGAG 3600  
 3601 ATTACAGGCGCCGCCACCAAGCCAGCTAATTTTTTGTATTTTAGTAGAGACAGGGTT 3660  
 3661 TCATCATGTAGCAGGATGGTCTCGATCTACTGACCTCATGATCTGCCTGCCTTGGCCTC 3720  
 3721 CCAAAGTGCTGGGATTACAGGCTTGAGCCACTGCACCCAGCCTACATCAGCCTTTTTTAA 3780  
 3781 AGGATTTTTCTGGCCGGGCATGGTGGCTGACACCTTAATTCAGCACTTTTGGGAGGCCG 3840  
 3841 AGGTGGGAGGATCACCTGAGGTGGGAATTCGAGACCAGCCTGACCAACATGTAGAAACA 3900  
 3901 CCCCATCTGTACTAAAAATACAAAAGTAGCCAGGCATGGTGGTGCATGCCTATAATGCCA 3960  
 3961 GCTACTCGCGAGGCTGAGGCAGGAGAATCCGTTGAACCCGGGAGGTGGAAGTTGCTGTGA 4020  
 4021 GCTGAGATGGAGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAACTCCGTCTCAAAAA 4080  
 4081 AAAAAAAGGGGGGGTTTCTGACGCACGGCCCTTGCACAAGCAATTCTTATTCCTGG 4140  
 4141 CATGCCTTCTGCTCTCTGTCCCTCTTTGCCTGGAGAAGTTCAATTTTCTTCTGAACAC 4200  
 4201 TCTTTACTTTGTATTTTGAGACAGGGTCTTGCTCTGTCAACAGTGCTGGAGTGGAGTGGT 4260  
 4261 GTGATCATAGCCCGACATCTGGGCTGAAGCCATCCTCCCAACTCAGCCTCCTGAGTAGC 4320

**Figure 1E**

4321	TGGGACTGCAAGCGCATGCCACCACAGATGGCTAATTTTACTTTTTTTGGAGATTTTG	4380
4381	CCACTGCACTCCAGCCTGGATGACAGAGCGAGATTCCATCTCAAAAAAAAAAAGAAAAA	4440
4441	TTTGTAATTTGTGTATATGTGTGTGGTGGCATTCCACAAGCATAGGAGCTATGCCAAC	4500
4501	TGTATCTCCTAGTGACTAGTATAAGACGTGGGTAGAAGTGCTCAAAAAACACACTTTGTG	4560
4561	TATTTTTTTATCAAGGCACCAGCAAAAAACAAAAACAAAAATCACACACGCGGCTGG	4620
4621	GCGCGGTGGCTCATGCCTGTAAACCCAGCACTTTGGGAGGCTGAGGCGGTTGGATCACGA	4680
4681	GGTCAAGAGATGGAGACCATCTGGCCAACGGTGAAACCCGCTCTCTACTAAAAATACA	4740
4741	AAAATTAGCTGGGCGTGGTGGTGTGCACCTGTAGTCACAGCTACTCAGGAGGCTGAGGCA	4800
4801	GAAGAATCACTTGAACCCAGGAGGCGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCAC	4860
4861	TCCAGCCTGGGCGACAGAGTGGGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAA	4920
4921	AAAAAAAAAAAA	4931

Figure 2A

		1	50
HNTTBMV1	(1)	-----	-----
caspase_recruitment_protein	(1)	MAGGAWGRLLACYLEFTKKKEELKEFOLLANKAHSRSSSGETPACPEKTS	GG
cryopyrin	(1)	-MASTRCKLARVLEDELDDVLLKKFKMHLEDPFOKGCPLPLRCCTEDKADH	
NOD1	(1)	-----MEEQGHSEMEITIPSESHPHIQLKSNR-----ELLVTH	
		51	100
HNTTBMV1	(1)	-----	-----
caspase_recruitment_protein	(51)	MEVASVLYVAQVGEORAWDLAHTWEOMGLRSLCAQAEAGAGHSFPFPYSP	
cryopyrin	(50)	VDLATLMIDFNGBEKAWAMAWIFAINRDLYEKAKRDEPKWGSNDARV	
NOD1	(34)	LRNTOCLVDN-----LLKNDYFSAEDAEIVCACPTQDPKVRKILDVLQ	
		101	150
HNTTBMV1	(1)	-----	-----
caspase_recruitment_protein	(101)	SEPHLGSPSQPTSTAVLMPWTHLPACCTGSESRVLRQLPDTSGRRWRRE	
cryopyrin	(100)	SN-----PVIICQEDSTBEWMGLIETLSRISTCKMKKDYRKIKYRK	
NOD1	(77)	SK-----GEE--VSEFFIYLLQQLADAYMDLRFWLLLEIGESP	
		151	200
HNTTBMV1	(1)	-----	-----
caspase_recruitment_protein	(151)	ISASHLYCAIPSSDHESPSCESPNAPTSTAVLGSWGSFPQPSLAPREQE	
cryopyrin	(141)	YMRSRFQCTEDRNARLG-----	
NOD1	(112)	SELHQSKVIVNLEFVSRYTQLR-----	
		201	250
HNTTBMV1	(1)	-----	-----
caspase_recruitment_protein	(201)	APGTQWPLDETSGIYYTEIREREREKSEKGRPPWAAVGTTPQAHSSLQP	
cryopyrin	(158)	-----	-----
NOD1	(135)	-----	-----
		251	300
HNTTBMV1	(1)	-----MPKNSKVTQREH	
caspase_recruitment_protein	(251)	HHHPWEPSVRESLCSTWPWKNEDFNOKFTOLLQRPHPRSQDPLVKRS	
cryopyrin	(158)	-----ESVSLNRYTRIRLKEHRSQQRREQLIAI	
NOD1	(135)	-----HHHGRUSKFFVLCYACKEELILEIYMDTIME	
		301	350
HNTTBMV1	(13)	SSEHVTESVADLLALEPVDYKQSVLNAC-----EAG-CKQKAVEE	
caspase_recruitment_protein	(300)	WPDYVEENRCHLEIRDLFGGLDTPR--IVTIQGAAGIGKSTLARQV	
cryopyrin	(189)	GKTKICESPVSPHKMELLFDDDEHSEFVH-TVVFQGAAGIGKTLARKM	
NOD1	(166)	LVGHSNESLGSNSLACTLDHTTGILNEQSETIFILGAGVGKSMILQRI	
		351	400
HNTTBMV1	(54)	ELDTEDRPAWNSKLOYTLAQIGFSVGLGNTWR--FPYLCOKNCGGAYLV	
caspase_recruitment_protein	(348)	KEAWGRGOLYGRFOHVFYFSCRELAQSUVVS--LAPLIGDGTATPAE	
cryopyrin	(238)	MLDWASGTLYQDRFDYFYTHCREVSLVITORS--LGLDLMSCCPDENPE	
NOD1	(216)	QSLWATGRLDAG-VKFFFFHRCRMFSCFVESDRLCLODILFPHYCYPERD	
		401	450
HNTTBMV1	(101)	EYLVLLITLIGILFFLELAVCORIRRGSTGVVWHYICPRLGGIGFSSCIVC	
caspase_recruitment_protein	(395)	---IRQILSEPERLLTLLDGVDEPGWVLCPPSSELCLHMSQ-PPADAL	
cryopyrin	(285)	---THKIVRKESTRLLPLMDGCFDELCARDEHICPLCHDWQK-AERGIL	
NOD1	(265)	EEBVFAPLIRFHVALETFDCLDELHSDLLSRVDDSSCPWE-PAHPLVL	
		451	500
HNTTBMV1	(151)	LFVGLYYNVIIIGWSIFYFFKSFQYPLPWSECPVVENGSVAUVVAECES	
caspase_recruitment_protein	(440)	LGSLIGKTLPLDASELTARTATLQMLIPSLQARWVEVLGFSESSRKEY	
cryopyrin	(330)	LSSLIRKKLLPLASLLITREVALEKQLHLLDHPRHVEILGFSEAKRKEY	
NOD1	(314)	LANLLSGKLLKASKLLTARTGIEVPROFIR---KKVLLRGFSFSLHAY	
		501	550
HNTTBMV1	(201)	ATTYFWYREALISDSSESSESGINMKMTCLLVAMSTVGMAYVKGIQSS	
caspase_recruitment_protein	(490)	FYRYFTDERQATRAFRLVKSINKELWALCLVPWVSWIACCLCOMKRKE	
cryopyrin	(380)	FFKYFSDBAQARAAFSLIQENEVLFMCFIPLVCWIVCTGLQOMESECK	
NOD1	(361)	ARRMFPERALQDRLLSOLEANPNLCSLCSVPLFCWTFRCFOHFRARFEG	
		551	600
HNTTBMV1	(250)	---GVMYFSSLPYVVLACFLVRC-----LLLRGAV	
caspase_recruitment_protein	(539)	--KLTLSKTTITLCHYLALQALQAP-----LGPQL	
cryopyrin	(429)	--SLAQTSKTTTAVYVEFLSSLLQPRGCS-----QBHGLCAHL	
NOD1	(411)	SPQIPDCMTLLTDVFLVTEVHLNRMQPSLVQRNTRSPVETLHAGRDTL	

601 650

DGLHMFIPKIDKMDPQVWREAATQVFFALGLGFGGVIAFSSYNKQDNN  
RDLCSLAAGBGWQKKTLPSPDLDKHKHGDGALYSTFLKMGITQEHF--IP  
DGLCSLAAGGIWQKILFEESDLRHNGLQKADVSFAFLNNIFQKEVD-CE  
CSLQGVAFRCMEKSLFVETQEEVQASGLQERDMOLGLRLALPELGGGDD

		651	700
	HNTTBM3Y1	(329) CHFDAAALVSFINFETSVLAATLVVFAVLGPKANIMNEKCVMEAEKILCYL	
	caspase_recruitment_protein	(617) LSYSFHILCFQEFFAAMS YVLEDEKGR-----GKHSNCIDILEKTLBAY	
	cryopyrin	(514) KFYSFHIMTFQEFFAAMYLLLEEKEGRNTMPSGRLKLPSSRDVTVLBNY	
	NOD1	(511) QSYEFFHLTLCAFFTAFFLVLLDDRVGTQELLRFFQDWMPPACAATTSCTVP	
		701	750
	HNTTBM3Y1	(379) NTVLSRDIIIEPHVNFSSHITTKDVMEMYNVIMTVKEDQF-----	
	caspase_recruitment_protein	(661) CTHGLRGASTITRFLGLLSDEGEREMENTIFHCRLSQGR---N--LMQW	
	cryopyrin	(564) CKKEKGYLLIFVVRFLFGLVNOERTSYLEKKILSCKISQOIRLELLKWLIEVK	
	NOD1	(561) PFLPFQCLQSGSPAREDLFKNKDHFQFTNFFLCGGLLSKA-----K	
		751	800
	HNTTBM3Y1	(418) SALLGLDPCLLLEDELDKSVQGTGLAIIAFTIEMTHFPASPEWSVMFELMLI	
	caspase_recruitment_protein	(704) MPSLQQLLEPHSLDESLLCLYETRNKIFLTQVMAHEEEMGMCVETDMELIV	
	cryopyrin	(614) AKAKKLOLQPSQLELFLFYCLYEMQEEEDFQVQAMDPFKKIEINLSTRMDHMY	
	NOD1	(601) OKLLRHLYPAAALRRKRKALWAHLSSRGYIKSLERVOVPSFNOVOAMP	
		801	850
	HNTTBM3Y1	(468) N-----	
	caspase_recruitment_protein	(754) CTFCIKFSREVKKLLQLEEGROHR-----SIWSPS	
	cryopyrin	(664) SSFCEIENCHRVESISLGLFLHNMPEKEEEEEKEGRHLDMVQCVLPSSSHAA	
	NOD1	(651) LFIWMLRCIMETQSQKVGQLAAR-----GICA	
		851	900
	HNTTBM3Y1	(469) -----LGLCSMIGIMAGITPTIIDTFKVPKEMFTVCCVFE	
	caspase_recruitment_protein	(783) MVLLFRWVPTDAYWQILFSVLKVTNRNKELDLSCNSLSHSAVKSCEKTL	
	cryopyrin	(714) CSHGLVNSHLLTSSEFCRGLFSVLSTISQSLELDELSDGFCMRVLCEITL	
	NOD1	(678) NYLIKLTICNACASADCSASFVLHHFPKRLALDLNNNNINQYGVREIQPCF	
		901	950
	HNTTBM3Y1	(504) AFLVGLLFVQVRSQNYFVIMFEDYSATLPTLLIVILENTAVAWIYCTKKFM	
	caspase_recruitment_protein	(833) RRPRCLLETLRLACCGLTAECDCKDLAFGLRANQTLTELDLSENVIMDAG	
	cryopyrin	(764) QHPGCNIRRLWLGRCGLSHECCFDISTVLSSNQKLVELDLSDNAICDFGI	
	NOD1	(728) SR----LTVLRLSVNQITDGGVRLVSEELTKYKIVTYLGLYNNQITDVGFA	
		951	1000
	HNTTBM3Y1	(554) QELTEMLG--FRPYRFYHYMWKFSVSLMAVITFASIIQLGVTPPGYSAW	
	caspase_recruitment_protein	(883) KHLQRLQROPSSKQLQRLQVSCGLTSECCQDLASVLSASPSLKEEDLQON	
	cryopyrin	(814) RLICVGLKHLNCLNKKLWLVSQCLTSACCQDLASVLSSTSHSLTRFYVGEN	
	NOD1	(774) RYVTKILLD-ECKGLTLHKLCKNKITITSECGKYLLALAVKNKSSISVEGMWEN	
		1001	1050
	HNTTBM3Y1	(602) IKEEAEERYLYFPNWAMALLTLTVMAITLPVPVFLVRHFHLLSDG----	
	caspase_recruitment_protein	(933) NLDDVGVRLCEGLRHHPACKLIRGLDOTTILSEMROEIRALEQEKPOLL	
	cryopyrin	(864) ALGDSGVATLCEKAKNPOCNLOKLG-VNSGLTSVCCSALSSVISTNONIT	
	NOD1	(823) QVGDECAKAFABALRN-HPSLTILSLASNGISIEGGKSLARALQON----	
		1051	1100
	HNTTBM3Y1	(648) -----SN--TLSSVSYK--K--GRMMKDISNLE	
	caspase_recruitment_protein	(983) IFSRKPKSVMTPIEGIDTGEYSNSTSLTKRQRLGSEAAASHVAQANLKLL	
	cryopyrin	(914) HLYLRGNTLGDGKIKLLCEGLLHDECKLOVLELDNCNLTSHCCWDLSTLL	
	NOD1	(868) -----ISLEILLWITQNEINDEVAESLAEM	
		1101	1150
	HNTTBM3Y1	(669) ENDETIRFILLSKMP-----EAPSEMPTHSRYLGPGSTSPLETSGNF	
	caspase_recruitment_protein	(1033) DVSKLIFPTAETAEESSPEVVPVELLQVESPASQGDITHTKPLGTDDDFWGP	
	cryopyrin	(964) TSSQSLRLKLSIGNN-----DLGDLGVMMFCEVLKQOCSLLQNLGLSEMYFN	
	NOD1	(893) KVNQTLKHLWLION-----QITAKGTALALCALQSNITGTEICLNG	
		1151	1200
	HNTTBM3Y1	(710) NGRYGSGLYLASTPESEL-----	
	caspase_recruitment_protein	(1083) TGPVATEVVDKEKNLYRVHPVAGSYRWPNTGLCFVVREAVTVIEIEFCVW	
	cryopyrin	(1011) ETKSALETQOEKPELTVVVEFSW	
	NOD1	(934) NLIKPEEAKVYDEDEKRIICE-----	
	Consensus	(1151) NGKASELL EKPEVF A	

Figure 2C

		1201	1250
	HNTTBM1	(728)	-----
caspase_recruitment_protein	(1133)	DQFLGEINPQHSWMVAGPLLDIKAEPGAVEAVHLPHFVALQGGHVDTSLF	
cryopyrin	(1035)	-----	
NOD1	(954)	-----	
		1251	1300
	HNTTBM1	(728)	-----
caspase_recruitment_protein	(1183)	QVAHFKEEGMLLEKPARVELHHIVLENPSFSPLGVLLKMIHNALRFIPVT	
cryopyrin	(1035)	-----	
NOD1	(954)	-----	
		1301	1350
	HNTTBM1	(728)	-----
caspase_recruitment_protein	(1233)	SVVLLYHRLHPPEEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVG	
cryopyrin	(1035)	-----	
NOD1	(954)	-----	
		1351	1400
	HNTTBM1	(728)	-----
caspase_recruitment_protein	(1283)	HLGSGIRLQVKDKKDETLVWEALVKPGDLMPATTLIPPACIAVPSPLDAP	
cryopyrin	(1035)	-----	
NOD1	(954)	-----	
		1401	1450
	HNTTBM1	(728)	-----
caspase_recruitment_protein	(1333)	QLLHFVDQYREQLIARVTSVEVVLDKLGQVLSQEQYERVLAEINTRPSQM	
cryopyrin	(1035)	-----	
NOD1	(954)	-----	
		1451	1497
	HNTTBM1	(728)	-----
caspase_recruitment_protein	(1383)	RKLFSLSQSWDRKCKDGLYQALKETHPHLIMELWEKGSKKGLPLSS	
cryopyrin	(1035)	-----	
NOD1	(954)	-----	

1201 1250 1251 1300 1301 1350 1351 1400 1401 1450 1451 1497



D0067 NP

Figure 3

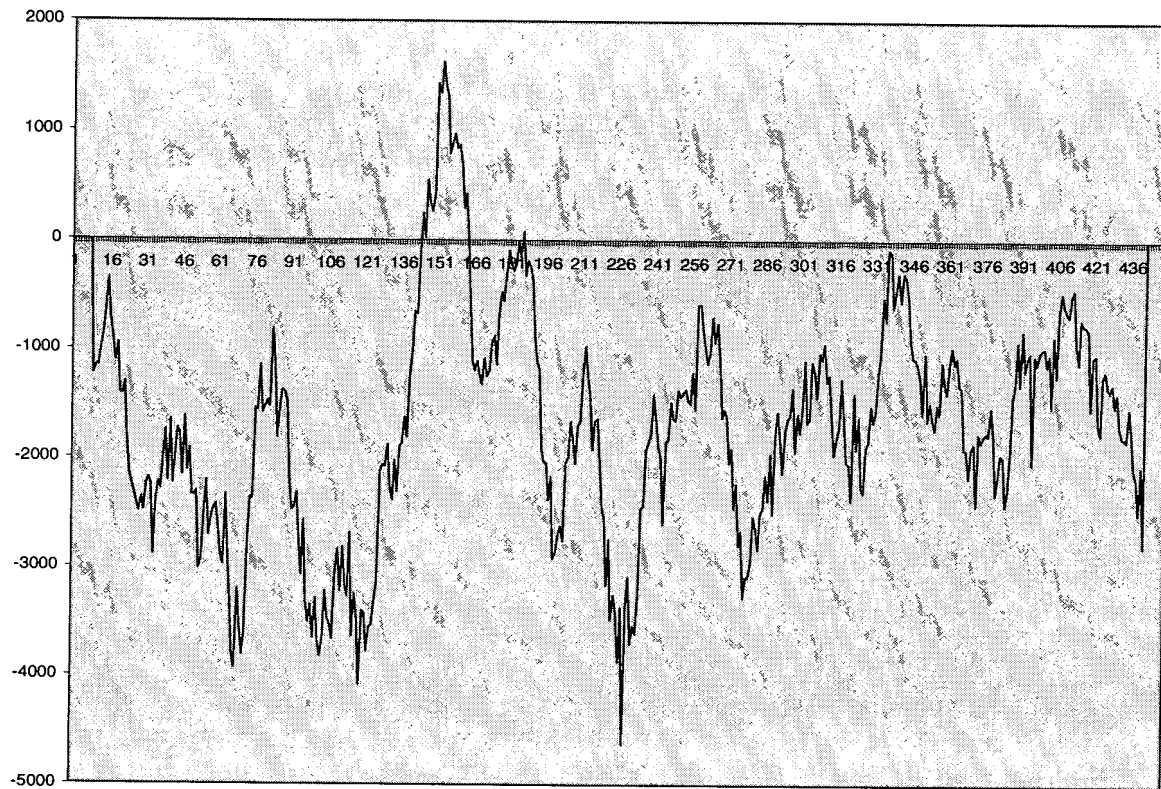
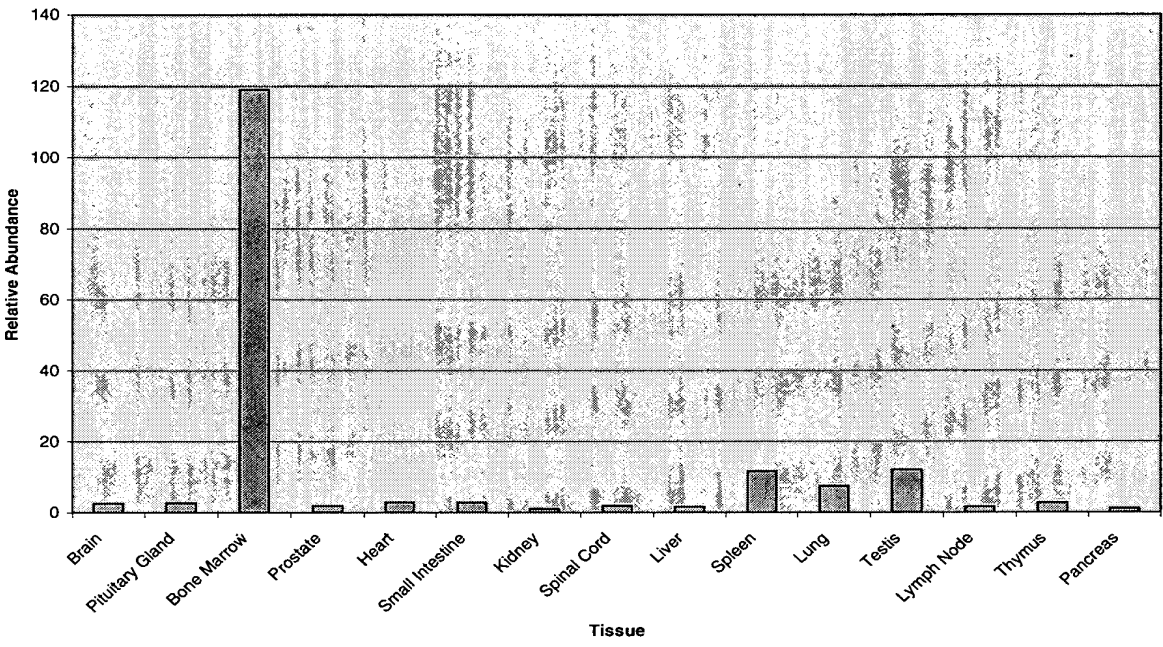


Figure 4



D0067 NP

Figure 5.

<u>Protein</u>	<u>Genbank ID</u>	<u>Percent Identity</u>	<u>Percent Similarity</u>
human caspase recruitment protein 7	gil10198209	35%	48%
human NOD caspase recruitment protein 4	gil5174617	25%	38%
human cryopyrin protein	gil17027237	51.7%	64.0%

12345678910111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913001301130213031304130513061307130813091310131113121313131413151316131713181319132013211322132313241325132613271328132913301331133213331334133513361337133813391340134113421343134413451346134713481349135013511352135313541355135613571358135913601361136213631364136513661367136813691370137113721373137413751376137713781379138013811382138313841385138613871388138913901391139213931394139513961397139813991400140114021403140414051406140714081409141014111412141314141415141614171418141914201421142214231424142514261427142814291430143114321433143414351436143714381439144014411442144314441445144614471448144914501451145214531454145514561457145814591460146114621463146414651466146714681469147014711472147314741475147614771478147914801481148214831484148514861487148814891490149114921493149414951496149714981499150015011502150315041505150615071508150915101511151215131514151515161517151815191520152115221523152415251526152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